## Sequence listing

5	Sequence No.: 1 Sequence length: 180 Sequence type: Nucleic acid Strandedness: Double Topology: Linear Sequence kind: cDNA to mRNA Sequence description																
10	004		omo	200		<b>m</b> a.											
			CTC														48
		Lys	Leu	Pro	_	Ser	Arg	Met	Pro		Cys	Glu	His	Met	Val	Glu	
	1	a			5					10					15		
			ACC														96
15	Ser	Pro	Thr	Cys	Ser	Gln	Met	Ser	Asn	Leu	Val	Cys	Gly	Thr	Asp	Gly	
				20					25					30			
			TAT														144
	Leu	Thr	Tyr	Thr	Asn	Glu	Cys	Gln	Leu	Cys	Leu	Ala	Arg	Ile	Lys	Thr	
			35					40					45				
20	AAA	CAG	GAC	ATC	CAG	ATC	ATG	AAA	GAT	GGC	AAA	TGC					180
	Lys	Gln	Asp	Ile	Gln	Ile	Met	Lys	Asp	Gly	Lys	Cys					
		50					55					60					
0.5																	

25 Sequence No.: 2

Sequence length: 398

Sequence type: Nucleic acid

Strandedness: Double Topology: Linear

30 Sequence kind: cDNA to mRNA

Origin:

Animal name: Homo sapiens

Cell kind: Stomach cancer tissue

Clone name: HP00839

35 Sequence characteristics:

Characterization code: CDS Existence position: 43..303

Sequence description

40 GCAGGCCCCA GCCAGCTCAG GCTACACTAT CCCAGGATCA GC ATG GCC GTC CGC

													Met 1	Ala	Val.	Arg	
	CAG	TGG	GTA	ATC	GCC	CTG	GCC	TTG	GCT	GCC	CTC	CTT	GTT	GTG	GAC	AGG	102
5	Gln	Trp	Val	Ile	Ala	Leu	Ala	Leu	Ala	Ala	Leu	Leu	Val	Val	Asp	Arg	
	5					10					15					20	
	GAA	GTG	CCA	GTG	GCA	GCA	GGA	AAG	CTC	CCT	TTC	TCA	AGA	ATG	CCC	ATC	150
	Glu	Val	Pro	Val	Ala	Ala	Gly	Lys	Leu	Pro	Phe	Ser	Arg	Met	Pro	Ile	
					25					30					35		
10	TGT	GAA	CAC	ATG	GTA	GAG	TCT	CCA	ACC	TGT	TCC	CAG	ATG	TCC	AAC	CTG	198
	Cys	Glu	His	Met	Val	Glu	Ser	Pro	Thr	Cys	Ser	Gln	Met	Ser	Asn	Leu	
				40					45					50			
		TGC															246
	Val	Cys		Thr	Asp	Gly	Leu	Thr	Tyr	Thr	Asn	Glu	Cys	Gln	Leu	Cys	
			55					60					65				
15		GCC															294
	Leu	Ala	Arg	Ile	Lys	Thr	Lys	Gln	Asp	Ile	Gln	Ile	Met	Lys	Asp	Gly	
		70					75					80					
		TGC	TGAT	`CCCA	CA G	GAGC	CACCI	°C AA	GCCA	TGAA	GTG	TCAG	CTG	GAGA	ACAG	TG	350
	Lys	Cys															
20	85																
	GTGG	GCAT	GG A	GAGG	ATAT	'G AC	ATGA	AATA	AAA	.GATC	CAG	CCCA	ACTG				398